

Supplementary Figures:

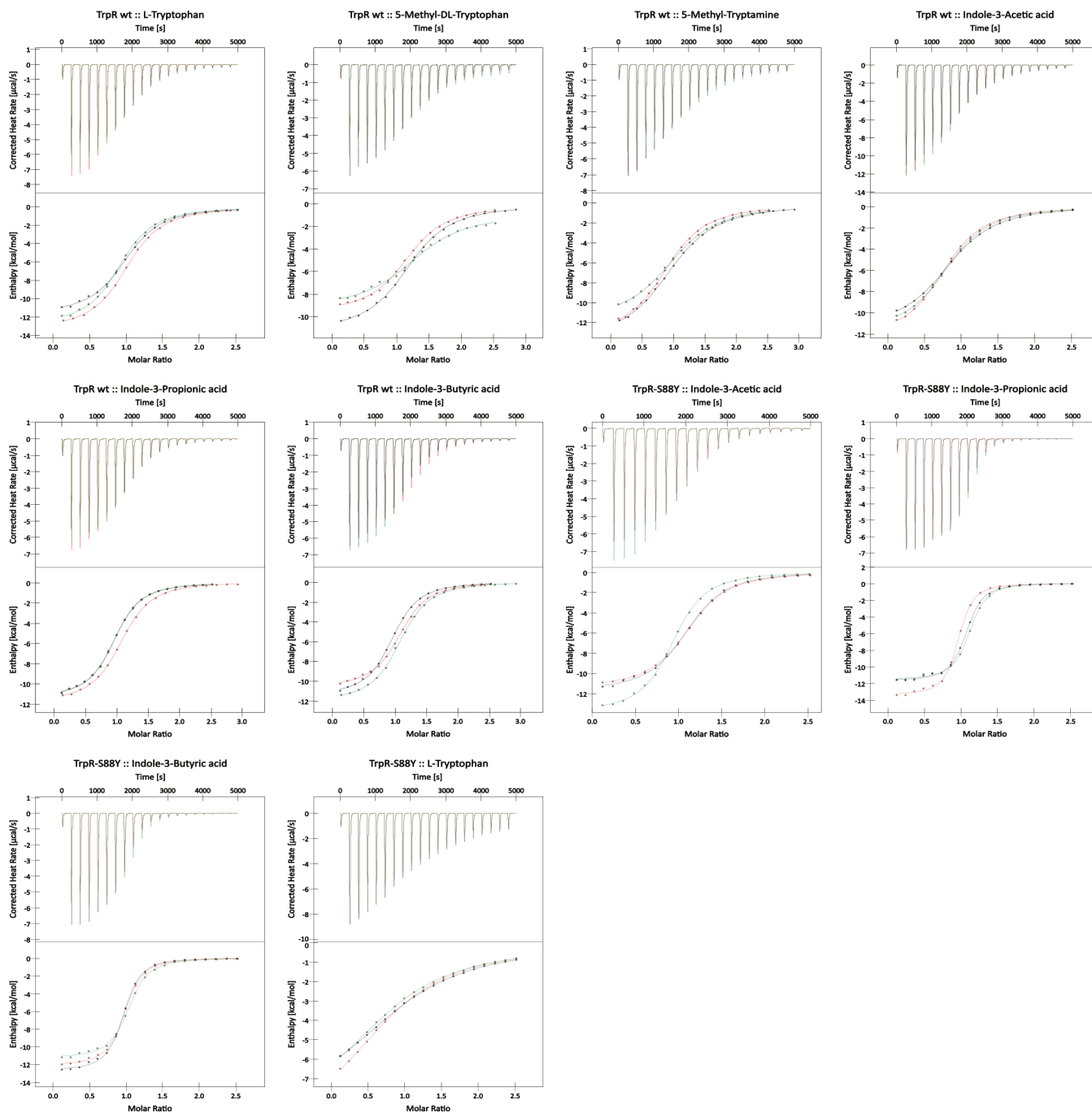


FIGURE S1: Analysis of binding to TrpR and the mutant TrpR-S88Y by ITC. Each plot shows three independent measurements.

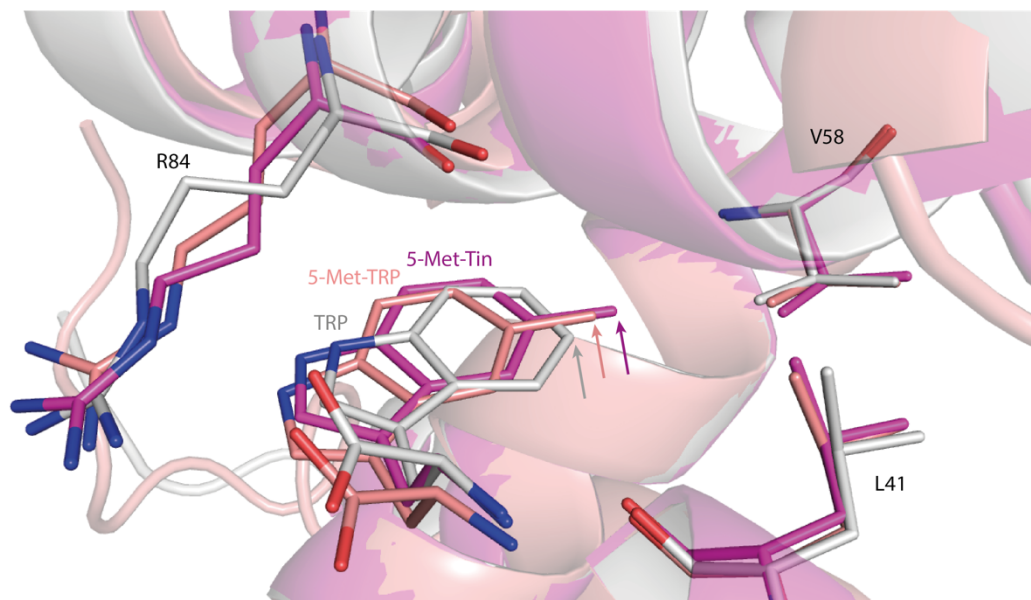


FIGURE S2: Packing of TRP (gray), 5-Met-TRP (salmon) and 5-Met-Tin (magenta) in the back of the binding pocket. The lacking stabilization at the 3'-substituent and the favorable packing of the methyl group is reflected in 5-Met-Tin being buried deepest in the pocket (arrows).

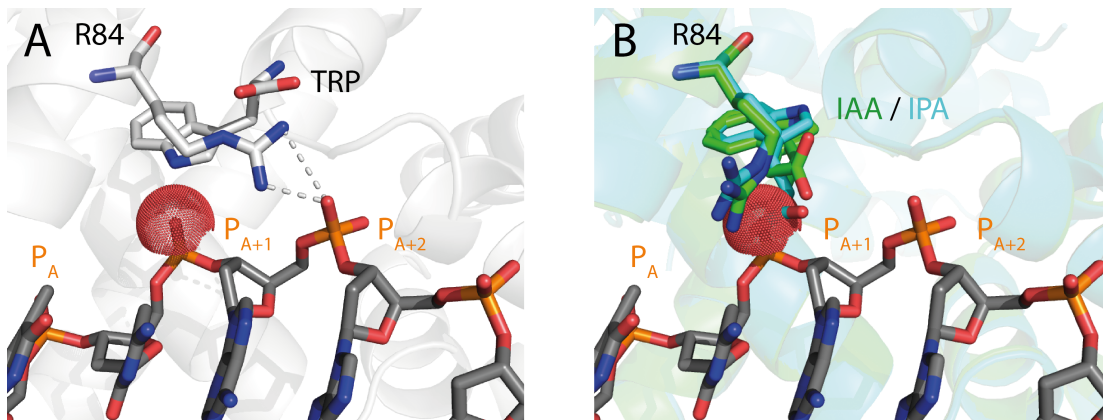


FIGURE S3: Interaction of TrpR with the Operator region of DNA with the native ligand tryptophan (A) and the pseudo-repressors (B) Indole-3-acetic acid (IAA) and Indole-3-propionic acid (IPA).

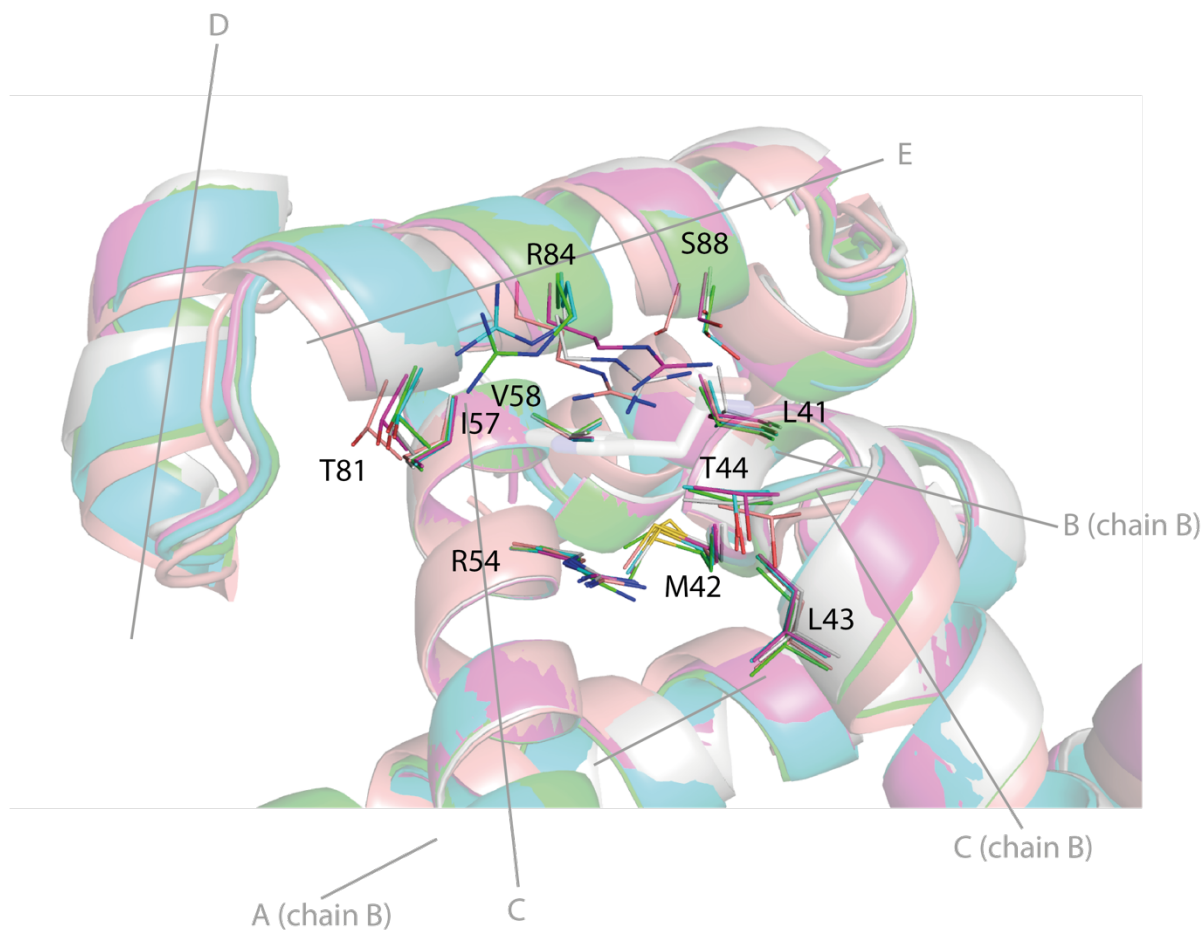


FIGURE S4: Superimposition (helix C) of TrpR binding different ligands (coloring as in Figure 1). Residues surrounding the ligand (for clarity only TRP shown here with transparency) shown as sticks; helical axes are indicated by letters. It is apparent that residues of the “central core” (helix B and C) like L41, M42, L43, R54, I57 and V58 show a low flexibility while residues of the “reading head region” (helix D and E) such as T81, R84 and S88 show more flexibility when accommodating the chemical nature of the different ligands. This is further reflected in the backbone variability of this region.

TABLE S1: Data collection and refinement statistics (molecular replacement) for structures elucidated in this study. Values for highest resolution shell are shown in brackets. The structures for TrpR :: IAA (6EJW) and TrpR-S88Y :: IAA (6EJZ) have been elucidated in another study.

	TrpR :: 5-Met-TRP (6F9K)	TrpR :: 5-Met-Tryptamine (6F7G)	TrpR :: IPA (6F7F)	TrpR-S88Y :: IPA (6FAL)
wavelength	0.92	1.00	1.00	0.98
Resolution range	20.88 - 1.41 (1.45 - 1.40)	33.10 - 1.66 (1.72 - 1.66)	40.92 - 2.13 (2.20 - 2.13)	35.87 - 1.20 (1.24 - 1.20)
Space group	P 43 2 2	P 1 2 1 1	P 43	P 1 2 1 1
Unit cell	53.15 53.15 90.83 90 90 90	35.35 55.55 66.99 90 98.82 90	81.84 81.84 70.57 90 90 90	36.07 45.25 60.67 90 104.02 90
Total reflections	222964 (21911)	198258 (16583)	341121 (24524)	363609 (28813)
Unique reflections	26306 (2544)	30265 (2707)	26212 (2523)	59053 (5462)
Multiplicity	8.50 (8.60)	6.60 (6.10)	13.00 (9.50)	6.20 (5.30)
Completeness (%)	99.53 (98.91)	96.71 (88.58)	99.52 (95.53)	98.96 (92.10)
Mean I/sigma(I)	14.94 (0.43)	15.44 (3.76)	12.38 (2.59)	18.89 (6.18)
Wilson B-factor	21.58	16.38	26.70	11.37
R-merge	0.08 (4.55)	0.24 (0.32)	0.17 (0.99)	0.06 (0.25)
R-meas	0.08 (4.84)	0.26 (0.36)	0.19 (1.04)	0.07 (0.28)
R-pim	0.03 (1.63)	0.10 (0.14)	0.05 (0.32)	0.03 (0.12)
CC1/2	1.00 (0.24)	0.84 (0.96)	1.00 (0.78)	1.00 (0.95)
CC*	1.00 (0.62)	0.95 (0.99)	1.00 (0.94)	1.00 (0.99)
Reflections used in refinement	26294 (2544)	29657 (2707)	26148 (2523)	59043 (5459)
Reflections used for R-free	1315 (127)	1481 (136)	1308 (126)	2953 (273)
R-work	0.19 (0.46)	0.19 (0.26)	0.17 (0.26)	0.16 (0.21)
R-free	0.20 (0.46)	0.23 (0.29)	0.23 (0.32)	0.18 (0.22)
CC(work)	0.96 (0.55)	0.95 (0.93)	0.97 (0.81)	0.95 (0.91)
CC(free)	0.96 (0.43)	0.93 (0.88)	0.93 (0.68)	0.94 (0.90)
Number of non-hydrogen atoms	1027	1995	3686	1870
macromolecules	877	1623	3306	1617
ligands	84	26	56	28
solvent	66	346	324	225